SEQUENCE LISTING

<110> Xia, Zhi-Qiang
      Costa, Michael A
      Davin, Laurence B
      Lewis, Norman G

<120> Recombinant Secoisolariciresinol Dehydrogenase, and
      Methods of Use

<130> WSUR116430

<140> 09/673,918
<141> 2000-10-23

<150> PCT/US99/08975
<151> 1999-04-23

<150> 60/082,977
<151> 1998-04-24

<160> 25

<170> PatentIn Ver. 2.0

<210> 1
<211> 819
<212> DNA
<213> Forsythia x intermedia

<220>
<221> CDS
<222> (1)..(819)

<400> 1

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atg cag ctt cga act gca ttc gca aga agg cta gaa gga aaa gtt gcc      48
Met Gln Leu Arg Thr Ala Phe Ala Arg Arg Leu Glu Gly Lys Val Ala
 1               5                  10                  15

ctt ata aca gga gga gcc agt gga att gga gaa acc aca gca aaa ctc      96
Leu Ile Thr Gly Gly Ala Ser Gly Ile Gly Glu Thr Thr Ala Lys Leu
                20                  25                  30

ttc tcc caa cat gga gcc aaa gtt gcc att gct gat gtc caa gat gaa     144
Phe Ser Gln His Gly Ala Lys Val Ala Ile Ala Asp Val Gln Asp Glu
         35                  40                  45

tta ggt cac tca gtt gtc gag gcc att ggc act tcc aat tcc acc tac     192
Leu Gly His Ser Val Val Glu Ala Ile Gly Thr Ser Asn Ser Thr Tyr
     50                  55                  60

atc cac tgt gat gtt act aat gaa gac ggt gtt aaa aat gcc gtg gac     240
Ile His Cys Asp Val Thr Asn Glu Asp Gly Val Lys Asn Ala Val Asp
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```
          65                  70                  75                  80

aac aca gtt tca acc tat gga aaa ctg gac att atg ttc agc aat gca    288
Asn Thr Val Ser Thr Tyr Gly Lys Leu Asp Ile Met Phe Ser Asn Ala
                85                  90                  95

gga att tct gat ccc aac agg ccc cgc atc ata gac aac gaa aaa gca    336
Gly Ile Ser Asp Pro Asn Arg Pro Arg Ile Ile Asp Asn Glu Lys Ala
            100                 105                 110

gac ttt gaa cgc gtt ctc agt gta aat gta acc gga gtt ttc cta tgc    384
Asp Phe Glu Arg Val Leu Ser Val Asn Val Thr Gly Val Phe Leu Cys
        115                 120                 125

atg aag cac gca gca cgt gtt atg att cca gca cgc agt ggc aac ata    432
Met Lys His Ala Ala Arg Val Met Ile Pro Ala Arg Ser Gly Asn Ile
    130                 135                 140

att tcc act gct agt tta agc tca act atg ggt ggt ggt tct tca cat    480
Ile Ser Thr Ala Ser Leu Ser Ser Thr Met Gly Gly Gly Ser Ser His
145                 150                 155                 160

gcc tat tgt ggt tca aag cat gct gtg tta gcc ctt act agg aat ctg    528
Ala Tyr Cys Gly Ser Lys His Ala Val Leu Ala Leu Thr Arg Asn Leu
                165                 170                 175

gca gtc gag ctc gga caa ttt ggc att agg gtt aat tgt ttg tct cct    576
Ala Val Glu Leu Gly Gln Phe Gly Ile Arg Val Asn Cys Leu Ser Pro
            180                 185                 190

ttc ggg ctt cct acg gct tta ggc aag aaa ttt tca ggg att aaa aat    624
Phe Gly Leu Pro Thr Ala Leu Gly Lys Lys Phe Ser Gly Ile Lys Asn
            195                 200                 205

gaa gaa gaa ttt gag aat gta ata aac ttt gcg gga aat ttg aaa ggt    672
Glu Glu Glu Phe Glu Asn Val Ile Asn Phe Ala Gly Asn Leu Lys Gly
    210                 215                 220

cca aaa ttt aat gtt gag gat gtt gcc aat gca gct ctt tat ctg gct    720
Pro Lys Phe Asn Val Glu Asp Val Ala Asn Ala Ala Leu Tyr Leu Ala
225                 230                 235                 240

agt gat gag gca aaa tac gtg agt gga cac aat ctg ttc att gat gga    768
Ser Asp Glu Ala Lys Tyr Val Ser Gly His Asn Leu Phe Ile Asp Gly
            245                 250                 255

ggg ttc agc gtc tgc aat tct gta atc aaa gtg ttc caa tat cca gat    816
Gly Phe Ser Val Cys Asn Ser Val Ile Lys Val Phe Gln Tyr Pro Asp
            260                 265                 270

tct                                                                 819
Ser
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<210> 2
<211> 273
<212> PRT
<213> Forsythia x intermedia

<400> 2
Met Gln Leu Arg Thr Ala Phe Ala Arg Arg Leu Glu Gly Lys Val Ala
  1               5                  10                  15

Leu Ile Thr Gly Gly Ala Ser Gly Ile Gly Glu Thr Thr Ala Lys Leu
              20                  25                  30

Phe Ser Gln His Gly Ala Lys Val Ala Ile Ala Asp Val Gln Asp Glu
          35                  40                  45

Leu Gly His Ser Val Val Glu Ala Ile Gly Thr Ser Asn Ser Thr Tyr
      50                  55                  60

Ile His Cys Asp Val Thr Asn Glu Asp Gly Val Lys Asn Ala Val Asp
 65                  70                  75                  80

Asn Thr Val Ser Thr Tyr Gly Lys Leu Asp Ile Met Phe Ser Asn Ala
              85                  90                  95

Gly Ile Ser Asp Pro Asn Arg Pro Arg Ile Ile Asp Asn Glu Lys Ala
             100                 105                 110

Asp Phe Glu Arg Val Leu Ser Val Asn Val Thr Gly Val Phe Leu Cys
         115                 120                 125

Met Lys His Ala Ala Arg Val Met Ile Pro Ala Arg Ser Gly Asn Ile
     130                 135                 140

Ile Ser Thr Ala Ser Leu Ser Ser Thr Met Gly Gly Gly Ser Ser His
145                 150                 155                 160

Ala Tyr Cys Gly Ser Lys His Ala Val Leu Ala Leu Thr Arg Asn Leu
             165                 170                 175

Ala Val Glu Leu Gly Gln Phe Gly Ile Arg Val Asn Cys Leu Ser Pro
             180                 185                 190

Phe Gly Leu Pro Thr Ala Leu Gly Lys Lys Phe Ser Gly Ile Lys Asn
         195                 200                 205

Glu Glu Glu Phe Glu Asn Val Ile Asn Phe Ala Gly Asn Leu Lys Gly
     210                 215                 220

Pro Lys Phe Asn Val Glu Asp Val Ala Asn Ala Ala Leu Tyr Leu Ala
225                 230                 235                 240

Ser Asp Glu Ala Lys Tyr Val Ser Gly His Asn Leu Phe Ile Asp Gly
```

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               245                    250                    255
      Gly Phe Ser Val Cys Asn Ser Val Ile Lys Val Phe Gln Tyr Pro Asp
                  260                    265                    270

      Ser
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<210> 3
<211> 831
<212> DNA
<213> Forsythia x intermedia

<220>
<221> CDS
<222> (1)..(831)

<400> 3

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atg gca gcc act tca cag gtt cta act gca atc gca aga agg cta gaa    48
Met Ala Ala Thr Ser Gln Val Leu Thr Ala Ile Ala Arg Arg Leu Glu
  1               5                  10                  15


gga aaa gtt gcc ctt ata aca gga gga gcc agt gga att gga gaa acc    96
Gly Lys Val Ala Leu Ile Thr Gly Gly Ala Ser Gly Ile Gly Glu Thr
               20                  25                  30


aca gca aaa ctc ttc tcc caa cat gga gcc aaa gtt gcc att gct gat    144
Thr Ala Lys Leu Phe Ser Gln His Gly Ala Lys Val Ala Ile Ala Asp
            35                  40                  45


gtc caa gat gaa tta ggt cac tca gtt gtc gag gcc att ggc act tcc    192
Val Gln Asp Glu Leu Gly His Ser Val Val Glu Ala Ile Gly Thr Ser
         50                  55                  60


aat tcc acc tac atc cac tgt gat gtt act aat gaa gac ggt gtt aaa    240
Asn Ser Thr Tyr Ile His Cys Asp Val Thr Asn Glu Asp Gly Val Lys
 65                  70                  75                  80


aat gcc gtg gac aac aca gtt tca acc tat gga aaa ctg gac att atg    288
Asn Ala Val Asp Asn Thr Val Ser Thr Tyr Gly Lys Leu Asp Ile Met
                 85                  90                  95


ttc agc aat gca gga att tct gat ccc aac agg ccc cgc atc ata gac    336
Phe Ser Asn Ala Gly Ile Ser Asp Pro Asn Arg Pro Arg Ile Ile Asp
               100                 105                 110


aac gaa aaa gca gac ttt gaa cgc gtt ttc agt gta aat gta acc gga    384
Asn Glu Lys Ala Asp Phe Glu Arg Val Phe Ser Val Asn Val Thr Gly
            115                 120                 125


gtt ttc cta tgc atg aag cac gca gca cgt gtt atg att cca gca cgc    432
Val Phe Leu Cys Met Lys His Ala Ala Arg Val Met Ile Pro Ala Arg
```

```
         130                      135                     140

agt ggc aac ata att tcc act gct agt tta agc tca act atg ggt ggt    480
Ser Gly Asn Ile Ile Ser Thr Ala Ser Leu Ser Ser Thr Met Gly Gly
145                 150                 155                 160

ggt tct tca cat gcc tat tgt ggt tca aag cat gct gtg tta ggc ctt    528
Gly Ser Ser His Ala Tyr Cys Gly Ser Lys His Ala Val Leu Gly Leu
                165                 170                 175

act agg aat ctg gca gtc gag ctc gga caa ttt ggc att agg gtt aat    576
Thr Arg Asn Leu Ala Val Glu Leu Gly Gln Phe Gly Ile Arg Val Asn
            180                 185                 190

tgt ttg tct cct ttc ggg ctt cct acg gct tta ggc aag aaa ttt tca    624
Cys Leu Ser Pro Phe Gly Leu Pro Thr Ala Leu Gly Lys Lys Phe Ser
            195                 200                 205

ggg att aaa aat gaa gaa gaa ttt gag aat gta ata aac ttt gcg gga    672
Gly Ile Lys Asn Glu Glu Glu Phe Glu Asn Val Ile Asn Phe Ala Gly
        210                 215                 220

aat ctg aaa ggt cca aaa ttt aat gtt gag gat gtt gcc aat gca gct    720
Asn Leu Lys Gly Pro Lys Phe Asn Val Glu Asp Val Ala Asn Ala Ala
225                 230                 235                 240

ctt tat ctg gct agt gat gag gca aaa tac gtg agt gga cac aat ctg    768
Leu Tyr Leu Ala Ser Asp Glu Ala Lys Tyr Val Ser Gly His Asn Leu
                245                 250                 255

ttc att gat gga ggg ttc agc gtc tgc aat tct gta atc aaa gtg ttc    816
Phe Ile Asp Gly Gly Phe Ser Val Cys Asn Ser Val Ile Lys Val Phe
                260                 265                 270

caa tat cca gat tct                                                831
Gln Tyr Pro Asp Ser
            275
```

<210> 4
<211> 277
<212> PRT
<213> Forsythia x intermedia

<400> 4

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Met Ala Ala Thr Ser Gln Val Leu Thr Ala Ile Ala Arg Arg Leu Glu
  1               5                  10                  15

Gly Lys Val Ala Leu Ile Thr Gly Gly Ala Ser Gly Ile Gly Glu Thr
            20                  25                  30

Thr Ala Lys Leu Phe Ser Gln His Gly Ala Lys Val Ala Ile Ala Asp
        35                  40                  45
```

```
Val Gln Asp Glu Leu Gly His Ser Val Val Glu Ala Ile Gly Thr Ser
    50                  55                  60

Asn Ser Thr Tyr Ile His Cys Asp Val Thr Asn Glu Asp Gly Val Lys
65                  70                  75                  80

Asn Ala Val Asp Asn Thr Val Ser Thr Tyr Gly Lys Leu Asp Ile Met
                85                  90                  95

Phe Ser Asn Ala Gly Ile Ser Asp Pro Asn Arg Pro Arg Ile Ile Asp
                100             105             110

Asn Glu Lys Ala Asp Phe Glu Arg Val Phe Ser Val Asn Val Thr Gly
        115                 120                 125

Val Phe Leu Cys Met Lys His Ala Ala Arg Val Met Ile Pro Ala Arg
    130                 135                 140

Ser Gly Asn Ile Ile Ser Thr Ala Ser Leu Ser Ser Thr Met Gly Gly
145                 150                 155                 160

Gly Ser Ser His Ala Tyr Cys Gly Ser Lys His Ala Val Leu Gly Leu
            165                 170                 175

Thr Arg Asn Leu Ala Val Glu Leu Gly Gln Phe Gly Ile Arg Val Asn
            180                 185                 190

Cys Leu Ser Pro Phe Gly Leu Pro Thr Ala Leu Gly Lys Lys Phe Ser
        195                 200                 205

Gly Ile Lys Asn Glu Glu Glu Phe Glu Asn Val Ile Asn Phe Ala Gly
    210                 215                 220

Asn Leu Lys Gly Pro Lys Phe Asn Val Glu Asp Val Ala Asn Ala Ala
225                 230                 235                 240

Leu Tyr Leu Ala Ser Asp Glu Ala Lys Tyr Val Ser Gly His Asn Leu
            245                 250                 255

Phe Ile Asp Gly Gly Phe Ser Val Cys Asn Ser Val Ile Lys Val Phe
            260                 265                 270

Gln Tyr Pro Asp Ser
        275
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<210> 5
<211> 819
<212> DNA
<213> Forsythia x intermedia

<220>
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<221> CDS
<222> (1)..(819)

<220>
<221> misc_feature
<222> (1)..(819)
<223> cDNA molecule encoding secoisolariciresinol dehydrogenase wherein
      Xaa = any amino acid

<400> 5
atg cag ctt cga act gca atc gca aga agg cta gaa gga aaa gtt gcc    48
Met Gln Leu Arg Thr Ala Ile Ala Arg Arg Leu Glu Gly Lys Val Ala
 1               5                  10                  15


ctt ata aca gga gga gcc agt gga gtt gga gaa gtc aca gca aaa ctc    96
Leu Ile Thr Gly Gly Ala Ser Gly Val Gly Glu Val Thr Ala Lys Leu
                20                  25                  30


ttc tcc caa cat gga gcc aaa gtt gcc att gct gat gtc caa gat gaa   144
Phe Ser Gln His Gly Ala Lys Val Ala Ile Ala Asp Val Gln Asp Glu
            35                  40                  45


tta ggt cac tca gtt gtc gag gcc att ggc cct tcc aat tcc acc tac   192
Leu Gly His Ser Val Val Glu Ala Ile Gly Pro Ser Asn Ser Thr Tyr
        50                  55                  60


atc cac tgc gat gtt act aat gaa gac ggt gtt aaa aat gcc gtg gac   240
Ile His Cys Asp Val Thr Asn Glu Asp Gly Val Lys Asn Ala Val Asp
 65                  70                  75                  80


aac aca gtt tca acc tat gga aaa ctg gac att atg ttc aac aat gca   288
Asn Thr Val Ser Thr Tyr Gly Lys Leu Asp Ile Met Phe Asn Asn Ala
                85                  90                  95


gga att tct gat ccc tac aag ccc cgg gtc ata gac aac gaa aaa gca   336
Gly Ile Ser Asp Pro Tyr Lys Pro Arg Val Ile Asp Asn Glu Lys Ala
            100                 105                 110


gac ttt gaa cgc gtt ctc agt gtn aat gtn acc gga gtt ttc cta ttt   384
Asp Phe Glu Arg Val Leu Ser Xaa Asn Xaa Thr Gly Val Phe Leu Phe
            115                 120                 125


atg aag cac gca gca cgc att atg gtt cca gca cga aat ggc tgc ata   432
Met Lys His Ala Ala Arg Ile Met Val Pro Ala Arg Asn Gly Cys Ile
        130                 135                 140


att tcc act gct agt tta agc tca act atg ggt ggt ggt tct tca cat   480
Ile Ser Thr Ala Ser Leu Ser Ser Thr Met Gly Gly Gly Ser Ser His
145                 150                 155                 160


gct tat tgt ggt gca aaa cat gct gta tta ggc ctt act agg aat ctg   528
Ala Tyr Cys Gly Ala Lys His Ala Val Leu Gly Leu Thr Arg Asn Leu
                165                 170                 175
```

```
gca gtc gag ctc gga caa ttt ggc att agg gtt aat tgt ttg tct cct    576
Ala Val Glu Leu Gly Gln Phe Gly Ile Arg Val Asn Cys Leu Ser Pro
            180             185             190

ttc ggg ctt cct acg cct cta gcc aag aaa ttt tca ggg att gaa aat    624
Phe Gly Leu Pro Thr Pro Leu Ala Lys Lys Phe Ser Gly Ile Glu Asn
            195             200             205

gat gta gac ttt gcg aat gca ata gaa cat gcg gga aat ctg aaa ggt    672
Asp Val Asp Phe Ala Asn Ala Ile Glu His Ala Gly Asn Leu Lys Gly
        210             215             220

aca aaa ttg agg att gag gat gtt gcc aat gca gct ctt ttt ctg gct    720
Thr Lys Leu Arg Ile Glu Asp Val Ala Asn Ala Ala Leu Phe Leu Ala
225             230             235             240

agt gat gag gca caa tat gtg agt gga caa aat ctg ttc atc gat gga    768
Ser Asp Glu Ala Gln Tyr Val Ser Gly Gln Asn Leu Phe Ile Asp Gly
            245             250             255

ggg ttc agc gtc tgc aat tct gca atc aaa atg ttc caa tat cca gac    816
Gly Phe Ser Val Cys Asn Ser Ala Ile Lys Met Phe Gln Tyr Pro Asp
            260             265             270

tct                                                                819
Ser
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<210> 6
<211> 273
<212> PRT
<213> Forsythia x intermedia

<220>
<221> misc_feature
<222> (1)..(273)
<223> Secoisolariciresinol dehydrogenase wherein Xaa = any amino acid

<400> 6
Met Gln Leu Arg Thr Ala Ile Ala Arg Arg Leu Glu Gly Lys Val Ala
 1               5                   10                  15

Leu Ile Thr Gly Gly Ala Ser Gly Val Gly Glu Val Thr Ala Lys Leu
                20                  25                  30

Phe Ser Gln His Gly Ala Lys Val Ala Ile Ala Asp Val Gln Asp Glu
            35                  40                  45

Leu Gly His Ser Val Val Glu Ala Ile Gly Pro Ser Asn Ser Thr Tyr
    50                  55                  60

Ile His Cys Asp Val Thr Asn Glu Asp Gly Val Lys Asn Ala Val Asp
```

		65			70			75			80

		65				70				75				80

```
              65                    70                    75                    80
Asn Thr Val Ser Thr Tyr Gly Lys Leu Asp Ile Met Phe Asn Asn Ala
                85                    90                    95

Gly Ile Ser Asp Pro Tyr Lys Pro Arg Val Ile Asp Asn Glu Lys Ala
            100                   105               110

Asp Phe Glu Arg Val Leu Ser Xaa Asn Xaa Thr Gly Val Phe Leu Phe
            115                   120               125

Met Lys His Ala Ala Arg Ile Met Val Pro Ala Arg Asn Gly Cys Ile
    130                   135               140

Ile Ser Thr Ala Ser Leu Ser Ser Thr Met Gly Gly Gly Ser Ser His
145                   150               155                   160

Ala Tyr Cys Gly Ala Lys His Ala Val Leu Gly Leu Thr Arg Asn Leu
            165                   170               175

Ala Val Glu Leu Gly Gln Phe Gly Ile Arg Val Asn Cys Leu Ser Pro
            180                   185               190

Phe Gly Leu Pro Thr Pro Leu Ala Lys Lys Phe Ser Gly Ile Glu Asn
            195                   200               205

Asp Val Asp Phe Ala Asn Ala Ile Glu His Ala Gly Asn Leu Lys Gly
            210                   215               220

Thr Lys Leu Arg Ile Glu Asp Val Ala Asn Ala Ala Leu Phe Leu Ala
225                   230               235                   240

Ser Asp Glu Ala Gln Tyr Val Ser Gly Gln Asn Leu Phe Ile Asp Gly
            245                   250               255

Gly Phe Ser Val Cys Asn Ser Ala Ile Lys Met Phe Gln Tyr Pro Asp
            260                   265               270

Ser
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<210> 7
<211> 831
<212> DNA
<213> Forsythia x intermedia

<220>
<221> CDS
<222> (1)..(831)

<400> 7
atg gcc agt act tca cag gtt cta act gca atc aca aga agg cta gaa   48

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Met Ala Ser Thr Ser Gln Val Leu Thr Ala Ile Thr Arg Arg Leu Glu
 1               5                  10                  15

gga aaa gtt gcc ctt ata aca gga gga gcc agt gga att gga gaa ttc    96
Gly Lys Val Ala Leu Ile Thr Gly Gly Ala Ser Gly Ile Gly Glu Phe
             20                  25                  30

aca gca aaa ctc ttc tcc caa cat gga gcc aaa gtt gcc att gct gat   144
Thr Ala Lys Leu Phe Ser Gln His Gly Ala Lys Val Ala Ile Ala Asp
             35                  40                  45

gtc caa gat gaa tta ggt cac tca gtt gtc gag gcc atc ggc act tcc   192
Val Gln Asp Glu Leu Gly His Ser Val Val Glu Ala Ile Gly Thr Ser
         50                  55                  60

aat tcc atc tac atc cac tgc gat gtt acc aat gaa gac gat gtt aaa   240
Asn Ser Ile Tyr Ile His Cys Asp Val Thr Asn Glu Asp Asp Val Lys
 65                  70                  75                  80

aat gcc gtg gac aac aca gtt tca acc tat gga aaa ctg gac att atg   288
Asn Ala Val Asp Asn Thr Val Ser Thr Tyr Gly Lys Leu Asp Ile Met
                 85                  90                  95

ttc aac aat gca gga att gct gac ccc aac aag ccc cgc atc gta gac   336
Phe Asn Asn Ala Gly Ile Ala Asp Pro Asn Lys Pro Arg Ile Val Asp
             100                 105                 110

aac gaa aaa gca gac ttt gaa cgc gtt ctc agc gta aat gta acc ggt   384
Asn Glu Lys Ala Asp Phe Glu Arg Val Leu Ser Val Asn Val Thr Gly
             115                 120                 125

gtt ttc cta tgc atg aag cac gca gca cgc gtt atg gtg cca gca cgc   432
Val Phe Leu Cys Met Lys His Ala Ala Arg Val Met Val Pro Ala Arg
     130                 135                 140

agt ggc agc ata att tcc act gct agc gta agc tca aca att ggt ggt   480
Ser Gly Ser Ile Ile Ser Thr Ala Ser Val Ser Ser Thr Ile Gly Gly
145                 150                 155                 160

gct gct tca cat gct tat tgt tgt tca aag cat gct gtg tta ggc ctt   528
Ala Ala Ser His Ala Tyr Cys Cys Ser Lys His Ala Val Leu Gly Leu
                 165                 170                 175

act agg aat ctg gca gtc gag ctc gga caa ttt ggc att agg gtt aat   576
Thr Arg Asn Leu Ala Val Glu Leu Gly Gln Phe Gly Ile Arg Val Asn
             180                 185                 190

tgt ttg gct cct tac gcg ctt gct acg cct tta gcc aag aaa ttt gta   624
Cys Leu Ala Pro Tyr Ala Leu Ala Thr Pro Leu Ala Lys Lys Phe Val
             195                 200                 205

ggg ctt gaa aat gac gaa gat ttg gag aat gca atg agc ctt atg gga   672
Gly Leu Glu Asn Asp Glu Asp Leu Glu Asn Ala Met Ser Leu Met Gly
```

```
              210                    215                    220
aat ctg aaa ggt aca aat ttg aag gct gag gac gtc gcc aat gca gct    720
Asn Leu Lys Gly Thr Asn Leu Lys Ala Glu Asp Val Ala Asn Ala Ala
225                 230                 235                 240

ctt tat ctg gca agt gat gag gca aaa tat gtg agt gga cac aat ctg    768
Leu Tyr Leu Ala Ser Asp Glu Ala Lys Tyr Val Ser Gly His Asn Leu
                    245                 250                 255

ttc att gat gga ggg ttc agc gtc tac aat tct gca atc aaa atg ttc    816
Phe Ile Asp Gly Gly Phe Ser Val Tyr Asn Ser Ala Ile Lys Met Phe
                    260                 265                 270

caa tat cca gac act                                                831
Gln Tyr Pro Asp Thr
            275


<210> 8
<211> 277
<212> PRT
<213> Forsythia x intermedia

<400> 8
Met Ala Ser Thr Ser Gln Val Leu Thr Ala Ile Thr Arg Arg Leu Glu
  1               5                  10                  15

Gly Lys Val Ala Leu Ile Thr Gly Gly Ala Ser Gly Ile Gly Glu Phe
                20                  25                  30

Thr Ala Lys Leu Phe Ser Gln His Gly Ala Lys Val Ala Ile Ala Asp
            35                  40                  45

Val Gln Asp Glu Leu Gly His Ser Val Val Glu Ala Ile Gly Thr Ser
        50                  55                  60

Asn Ser Ile Tyr Ile His Cys Asp Val Thr Asn Glu Asp Asp Val Lys
 65                  70                  75                  80

Asn Ala Val Asp Asn Thr Val Ser Thr Tyr Gly Lys Leu Asp Ile Met
                85                  90                  95

Phe Asn Asn Ala Gly Ile Ala Asp Pro Asn Lys Pro Arg Ile Val Asp
                100                 105                 110

Asn Glu Lys Ala Asp Phe Glu Arg Val Leu Ser Val Asn Val Thr Gly
            115                 120                 125

Val Phe Leu Cys Met Lys His Ala Ala Arg Val Met Val Pro Ala Arg
        130                 135                 140

Ser Gly Ser Ile Ile Ser Thr Ala Ser Val Ser Ser Thr Ile Gly Gly
```

```
              145                150                155                160
        Ala Ala Ser His Ala Tyr Cys Cys Ser Lys His Ala Val Leu Gly Leu
                        165                170                175

        Thr Arg Asn Leu Ala Val Glu Leu Gly Gln Phe Gly Ile Arg Val Asn
                    180                185                190

        Cys Leu Ala Pro Tyr Ala Leu Ala Thr Pro Leu Ala Lys Lys Phe Val
                195                200                205

        Gly Leu Glu Asn Asp Glu Asp Leu Glu Asn Ala Met Ser Leu Met Gly
            210                215                220

        Asn Leu Lys Gly Thr Asn Leu Lys Ala Glu Asp Val Ala Asn Ala Ala
        225                230                235                240

        Leu Tyr Leu Ala Ser Asp Glu Ala Lys Tyr Val Ser Gly His Asn Leu
                        245                250                255

        Phe Ile Asp Gly Gly Phe Ser Val Tyr Asn Ser Ala Ile Lys Met Phe
                    260                265                270

        Gln Tyr Pro Asp Thr
                275


<210> 9
<211> 828
<212> DNA
<213> Forsythia x intermedia

<220>
<221> CDS
<222> (1)..(828)

<400> 9
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Met Ala Thr Ser Gln Leu Arg Thr Ala Phe Ala Arg Arg Leu Glu Gly
  1               5                  10                  15

aaa gtt gcc ctt ata aca gga gga gcc agt gga gtt gga gaa gtc aca    96
Lys Val Ala Leu Ile Thr Gly Gly Ala Ser Gly Val Gly Glu Val Thr
                20                  25                  30

gca aaa ctc ttc tcc caa cat gga gcc aaa gtt gcc att gct gat gtc   144
Ala Lys Leu Phe Ser Gln His Gly Ala Lys Val Ala Ile Ala Asp Val
            35                  40                  45

caa gat gaa tta ggt cac tca gtt gtc gag gcc att ggc ctt tcc aat   192
Gln Asp Glu Leu Gly His Ser Val Val Glu Ala Ile Gly Leu Ser Asn
        50                  55                  60
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```
tcc acc tac atc cac tgc gat gtt act aat gaa gac ggt gtt aaa aat      240
Ser Thr Tyr Ile His Cys Asp Val Thr Asn Glu Asp Gly Val Lys Asn
 65                  70                  75                  80

gcc gtg gac aac aca gtt tca acc tat gga aaa ctg gac att atg ttc      288
Ala Val Asp Asn Thr Val Ser Thr Tyr Gly Lys Leu Asp Ile Met Phe
                 85                  90                  95

aac aat gca gga att tct gat ccc tac aag ccc cgg gtc ata gac aac      336
Asn Asn Ala Gly Ile Ser Asp Pro Tyr Lys Pro Arg Val Ile Asp Asn
                100                 105                 110

gaa aaa gca gac ttt gaa cgc gtt ctc agt gtt aat gta acc gga gtt      384
Glu Lys Ala Asp Phe Glu Arg Val Leu Ser Val Asn Val Thr Gly Val
            115                 120                 125

ttc cta ttt atg aag cac gca gca cgc att atg gtt cca gca cga agt      432
Phe Leu Phe Met Lys His Ala Ala Arg Ile Met Val Pro Ala Arg Ser
        130                 135                 140

ggc tgc ata att tcc act gct agt tta agc tca act atg ggt ggt ggt      480
Gly Cys Ile Ile Ser Thr Ala Ser Leu Ser Ser Thr Met Gly Gly Gly
145                 150                 155                 160

tct tca cat gct tat tgt ggt tca aag cat gct gta tta ggc ctt act      528
Ser Ser His Ala Tyr Cys Gly Ser Lys His Ala Val Leu Gly Leu Thr
                165                 170                 175

agg aat ctg gca gtc gag ctc gga caa ttt ggc att agg gtt aat tgt      576
Arg Asn Leu Ala Val Glu Leu Gly Gln Phe Gly Ile Arg Val Asn Cys
            180                 185                 190

ttg tct cct ttc ggg ctt cct acg cct tta gcc aag aaa ttt aca ggg      624
Leu Ser Pro Phe Gly Leu Pro Thr Pro Leu Ala Lys Lys Phe Thr Gly
            195                 200                 205

att gaa aat gat gaa gac ttg gcg aat gga ata gaa cgt gcg gga aat      672
Ile Glu Asn Asp Glu Asp Leu Ala Asn Gly Ile Glu Arg Ala Gly Asn
    210                 215                 220

ctg aaa ggt aca aaa ttg agg att gag gat gtt gcc aat gca gct ctt      720
Leu Lys Gly Thr Lys Leu Arg Ile Glu Asp Val Ala Asn Ala Ala Leu
225                 230                 235                 240

ttt ctg gct agt gat gag gca caa tat gtg agt gga caa aat ctg ttc      768
Phe Leu Ala Ser Asp Glu Ala Gln Tyr Val Ser Gly Gln Asn Leu Phe
            245                 250                 255

atc gat gga ggg ttc agc gtc tgc aat tct gca atc aaa ttg ttc caa      816
Ile Asp Gly Gly Phe Ser Val Cys Asn Ser Ala Ile Lys Leu Phe Gln
            260                 265                 270

tat cca gac tct                                                      828
Tyr Pro Asp Ser
```

Tyr Pro Asp Ser
        275

<210> 10
<211> 276
<212> PRT
<213> Forsythia x intermedia

<400> 10
Met Ala Thr Ser Gln Leu Arg Thr Ala Phe Ala Arg Arg Leu Glu Gly
 1   5   10   15

Lys Val Ala Leu Ile Thr Gly Gly Ala Ser Gly Val Gly Glu Val Thr
                20   25   30

Ala Lys Leu Phe Ser Gln His Gly Ala Lys Val Ala Ile Ala Asp Val
            35   40   45

Gln Asp Glu Leu Gly His Ser Val Val Glu Ala Ile Gly Leu Ser Asn
        50   55   60

Ser Thr Tyr Ile His Cys Asp Val Thr Asn Glu Asp Gly Val Lys Asn
 65   70   75   80

Ala Val Asp Asn Thr Val Ser Thr Tyr Gly Lys Leu Asp Ile Met Phe
                85   90   95

Asn Asn Ala Gly Ile Ser Asp Pro Tyr Lys Pro Arg Val Ile Asp Asn
            100   105   110

Glu Lys Ala Asp Phe Glu Arg Val Leu Ser Val Asn Val Thr Gly Val
        115   120   125

Phe Leu Phe Met Lys His Ala Ala Arg Ile Met Val Pro Ala Arg Ser
    130   135   140

Gly Cys Ile Ile Ser Thr Ala Ser Leu Ser Ser Thr Met Gly Gly Gly
145   150   155   160

Ser Ser His Ala Tyr Cys Gly Ser Lys His Ala Val Leu Gly Leu Thr
                165   170   175

Arg Asn Leu Ala Val Glu Leu Gly Gln Phe Gly Ile Arg Val Asn Cys
            180   185   190

Leu Ser Pro Phe Gly Leu Pro Thr Pro Leu Ala Lys Lys Phe Thr Gly
            195   200   205

Ile Glu Asn Asp Glu Asp Leu Ala Asn Gly Ile Glu Arg Ala Gly Asn
    210   215   220

Leu Lys Gly Thr Lys Leu Arg Ile Glu Asp Val Ala Asn Ala Ala Leu

```
              225                  230                  235                  240

              Phe Leu Ala Ser Asp Glu Ala Gln Tyr Val Ser Gly Gln Asn Leu Phe
                           245                  250                  255

              Ile Asp Gly Gly Phe Ser Val Cys Asn Ser Ala Ile Lys Leu Phe Gln
                        260                  265                  270

              Tyr Pro Asp Ser
                      275
```

```
<210> 11
<211> 21
<212> PRT
<213> Forsythia x intermedia

<220>
<221> PEPTIDE
<222> (1)..(21)
<223> N-terminal peptide of F. intermedia
      secoisolariciresinol protein wherein Xaa at
      positions 3, 12 and 20 represents an unidentified
      amino acid residue

<400> 11
Gln Val Xaa Thr Ala Ile Ala Arg Asp Leu Glu Xaa Lys Val Ala Leu
  1                   5                   10                  15

Ile Thr Gly Xaa Ala
              20
```

```
<210> 12
<211> 17
<212> PRT
<213> Forsythia x intermedia

<400> 12
Val Ala Leu Ile Thr Gly Gly Ala Ser Gly Ile Gly Glu Thr Thr Ala
  1                   5                   10                  15

Lys
```

```
<210> 13
<211> 15
<212> PRT
<213> Forsythia x intermedia

<400> 13
Leu Asn Ile Met Phe Ser Asn Ala Gly Ile Ser Asp Pro Asn Lys
```

```
<210> 14
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
      oligonucleotide

<220>
<221> misc_feature
<222> (1)..(20)
<223> PCR primer wherein n at positions 3, 9, 15 and 18
      represents inosine

<400> 14
ggnathggng aracnacngc                                        20


<210> 15
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
      oligonucleotide

<220>
<221> misc_feature
<222> (1)..(20)
<223> PCR primer wherein n at positions 3 and  9
      represents inosine

<400> 15
ccngcrttng araacatdat'                                       20


<210> 16
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
      oligonucleotide

<220>
<221> misc_feature
<222> (1)..(20)
```

<223> PCR primer wherein n at positions 3 and 9
      represents inosine

<400> 16
ccngcrttnc traacatdat   20

<210> 17
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
      oligonucleotide

<220>
<221> misc_feature
<222> (1)..(20)
<223> PCR primer

<400> 17
attccgctag attgcattga   20

<210> 18
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
      oligonucleotide

<220>
<221> misc_feature
<222> (1)..(20)
<223> PCR primer wherein n at positions 3 and 9
      represent inosine

<400> 18
ccngcrttnc traacatdat   20

<210> 19
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
      oligonucleotide

```
<220>
<221> misc_feature
<222> (1)..(20)
<223> T7 PCR primer

<400> 19
aattaaccct cactaaaggg                                                 20


<210> 20
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
      oligonucleotide

<220>
<221> misc_feature
<222> (1)..(23)
<223> PCR primer

<400> 20
cagcttcgaa ctgcattcgc aag                                             23


<210> 21
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
      oligonucleotide

<220>
<221> misc_feature
<222> (1)..(22)
<223> T7 PCR primer

<400> 21
cgggatatca ctcagcataa tg                                              22


<210> 22
<211> 816
<212> DNA
<213> Forsythia x intermedia

<220>
<221> CDS
<222> (1)..(816)
```

<400> 22

```
cag ctt cga act gca ttc gca aga agg cta gaa gga aaa gtt gcc ctt      48
Gln Leu Arg Thr Ala Phe Ala Arg Arg Leu Glu Gly Lys Val Ala Leu
  1               5                  10                  15

ata aca gga gga gcc agt gga att gga gaa acc aca gca aaa ctc ttc      96
Ile Thr Gly Gly Ala Ser Gly Ile Gly Glu Thr Thr Ala Lys Leu Phe
                 20                  25                  30

tcc caa cat gga gcc aaa gtt gcc att gct gat gtc caa gat gaa tta     144
Ser Gln His Gly Ala Lys Val Ala Ile Ala Asp Val Gln Asp Glu Leu
             35                  40                  45

ggt cac tca gtt gtc gag gcc att ggc act tcc aat tcc acc tac atc     192
Gly His Ser Val Val Glu Ala Ile Gly Thr Ser Asn Ser Thr Tyr Ile
         50                  55                  60

cac tgt gat gtt act aat gaa gac ggt gtt aaa aat gcc gtg gac aac     240
His Cys Asp Val Thr Asn Glu Asp Gly Val Lys Asn Ala Val Asp Asn
 65                  70                  75                  80

aca gtt tca acc tat gga aaa ctg gac att atg ttc agc aat gca gga     288
Thr Val Ser Thr Tyr Gly Lys Leu Asp Ile Met Phe Ser Asn Ala Gly
                 85                  90                  95

att tct gat ccc aac agg ccc cgc atc ata gac aac gaa aaa gca gac     336
Ile Ser Asp Pro Asn Arg Pro Arg Ile Ile Asp Asn Glu Lys Ala Asp
            100                 105                 110

ttt gaa cgc gtt ctc agt gta aat gta acc gga gtt ttc cta tgc atg     384
Phe Glu Arg Val Leu Ser Val Asn Val Thr Gly Val Phe Leu Cys Met
            115                 120                 125

aag cac gca gca cgt gtt atg att cca gca cgc agt ggc aac ata att     432
Lys His Ala Ala Arg Val Met Ile Pro Ala Arg Ser Gly Asn Ile Ile
        130                 135                 140

tcc act gct agt tta agc tca act atg ggt ggt ggt tct tca cat gcc     480
Ser Thr Ala Ser Leu Ser Ser Thr Met Gly Gly Gly Ser Ser His Ala
145                 150                 155                 160

tat tgt ggt tca aag cat gct gtg tta gcc ctt act agg aat ctg gca     528
Tyr Cys Gly Ser Lys His Ala Val Leu Ala Leu Thr Arg Asn Leu Ala
                165                 170                 175

gtc gag ctc gga caa ttt ggc att agg gtt aat tgt ttg tct cct ttc     576
Val Glu Leu Gly Gln Phe Gly Ile Arg Val Asn Cys Leu Ser Pro Phe
            180                 185                 190

ggg ctt cct acg gct tta ggc aag aaa ttt tca ggg att aaa aat gaa     624
Gly Leu Pro Thr Ala Leu Gly Lys Lys Phe Ser Gly Ile Lys Asn Glu
            195                 200                 205
```

```
gaa gaa ttt gag aat gta ata aac ttt gcg gga aat ttg aaa ggt cca    672
Glu Glu Phe Glu Asn Val Ile Asn Phe Ala Gly Asn Leu Lys Gly Pro
    210             215             220

aaa ttt aat gtt gag gat gtt gcc aat gca gct ctt tat ctg gct agt    720
Lys Phe Asn Val Glu Asp Val Ala Asn Ala Ala Leu Tyr Leu Ala Ser
225             230             235             240

gat gag gca aaa tac gtg agt gga cac aat ctg ttc att gat gga ggg    768
Asp Glu Ala Lys Tyr Val Ser Gly His Asn Leu Phe Ile Asp Gly Gly
            245             250             255

ttc agc gtc tgc aat tct gta atc aaa gtg ttc caa tat cca gat tct    816
Phe Ser Val Cys Asn Ser Val Ile Lys Val Phe Gln Tyr Pro Asp Ser
            260             265             270
```

```
<210> 23
<211> 272
<212> PRT
<213> Forsythia x intermedia

<400> 23
Gln Leu Arg Thr Ala Phe Ala Arg Arg Leu Glu Gly Lys Val Ala Leu
  1               5              10                      15

Ile Thr Gly Gly Ala Ser Gly Ile Gly Glu Thr Thr Ala Lys Leu Phe
            20              25                      30

Ser Gln His Gly Ala Lys Val Ala Ile Ala Asp Val Gln Asp Glu Leu
        35              40                      45

Gly His Ser Val Val Glu Ala Ile Gly Thr Ser Asn Ser Thr Tyr Ile
      50              55              60

His Cys Asp Val Thr Asn Glu Asp Gly Val Lys Asn Ala Val Asp Asn
  65              70              75                      80

Thr Val Ser Thr Tyr Gly Lys Leu Asp Ile Met Phe Ser Asn Ala Gly
                85              90                      95

Ile Ser Asp Pro Asn Arg Pro Arg Ile Ile Asp Asn Glu Lys Ala Asp
            100             105             110

Phe Glu Arg Val Leu Ser Val Asn Val Thr Gly Val Phe Leu Cys Met
        115             120             125

Lys His Ala Ala Arg Val Met Ile Pro Ala Arg Ser Gly Asn Ile Ile
    130             135             140

Ser Thr Ala Ser Leu Ser Ser Thr Met Gly Gly Gly Ser Ser His Ala
145             150             155             160
```

```
Tyr Cys Gly Ser Lys His Ala Val Leu Ala Leu Thr Arg Asn Leu Ala
            165             170             175

Val Glu Leu Gly Gln Phe Gly Ile Arg Val Asn Cys Leu Ser Pro Phe
            180             185             190

Gly Leu Pro Thr Ala Leu Gly Lys Lys Phe Ser Gly Ile Lys Asn Glu
        195             200             205

Glu Glu Phe Glu Asn Val Ile Asn Phe Ala Gly Asn Leu Lys Gly Pro
    210             215             220

Lys Phe Asn Val Glu Asp Val Ala Asn Ala Ala Leu Tyr Leu Ala Ser
225             230             235             240

Asp Glu Ala Lys Tyr Val Ser Gly His Asn Leu Phe Ile Asp Gly Gly
            245             250             255

Phe Ser Val Cys Asn Ser Val Ile Lys Val Phe Gln Tyr Pro Asp Ser
            260             265             270
```

```
<210> 24
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
     oligonucleotide

<220>
<221> misc_feature
<222> (1)..(33)
<223> PCR primer

<400> 24
acatatgcag cttcgaactg cattcgcaag aag                                33


<210> 25
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
     oligonucleotide

<220>
<221> misc_feature
<222> (1)..(33)
```

<223> PCR primer

<400> 25
catatgggca gacatgttac atgatcaatt gca   33